Patent claims:

1. A degenerate primer constituent from the group consisting of

A-01f : gcsmrsgcstgg (Seq. ID NO. 1)
B-01f : ggsctsccscc (Seq. ID NO. 2)
B-01r : ggsggsagscc (Seq. ID NO. 3)
C-01r : ggncgcwbsgg (Seq. ID NO. 4)
A-01f : gcnmrrgcntgg (Seq. ID NO. 5)
B-01f : ggnytnccncc (Seq. ID NO. 6)
B-01r : ggnggnarncc (Seq. ID NO. 7)
C-01r : gwngwrtccca (Seq. ID NO. 8)
A-01f : gcntggrynga (Seq. ID NO. 9)
B-01f : ggnytsccncc (Seq. ID NO. 10)
B-01r : ggnggsarncc (Seq. ID NO. 11)
C-01r : swnswrtccca (Seq. ID NO. 12).

2. A process for preparing protein sequences which are required for constructing the activity of a nitrile hydratase, such that
a) a metagenome DNA library of a habitat is prepared,
b) this library is contacted with in each case at least one forward(f) primer and one reverse(r) primer exhibiting a degenerate nucleic acid sequence as claimed in claim 1,
c) a PCR is carried out using these primers,
d) the full-length sequences of the nucleic acids encoding protein sequences which are required for constructing the activity of a nitrile hydratase are generated from the part sequences which are obtained, and
e) these full-length sequences are cloned into a host organism and expressed.

3. The process as claimed in claim 2, characterized in that

in each case primer pairs composed of primers exhibiting the nucleic acid sequences A-01f and B-01r or C-01r and also B-01f and C-01r are used in the PCR.

4. The process as claimed in claim 2 and/or 3, characterized in that nucleic acid sequences selected from the group consisting of:

GCCAAGGTCGTC	(Seq. ID NO. 13)
GGCCGGTCCTG	(Seq. ID NO. 14)
TCCTTGTACCAGGTC	(Seq. ID NO. 15)
GCCCGCC	(Seq. ID NO. 16)
GGCGCTAATGTTGTT	(Seq. ID NO. 17)
TGGCCGGTTCTG	(Seq. ID NO. 18)
CAAATTCTTTATACCAAGTC	(Seq. ID NO. 19)
CCATATATCGCATTTCAGCT	(Seq. ID NO. 20)
GGTCGTGGCCAAG	(Seq. ID NO. 21)
GGCCGGTCCTG	(Seq. ID NO. 22)
TCCTTGTACCAGGTC	(Seq. ID NO. 23)
GCGCATTTCGGCG	(Seq. ID NO. 24)

are placed upstream of the degenerate nucleic acid sequences.

5. The process as claimed in one or more of the preceding claims 2 to 4, characterized in that use is made of primers which are selected from the group consisting of

GCCAAGGTCGTCgcsmrsgcstgg	(Seq. ID NO. 25)
GGCCGGTCCTGggsctsccscc	(Seq. ID NO. 26)
TCCTTGTACCAGGTCggsggsagscc	(Seq. ID NO. 27)
GCCCGCCggncgcwbsgg	(Seq. ID NO. 28)
GGCGCTAAAGTTGTTgcnmrrgcntgg	(Seq. ID NO. 29)
TGGCCGGTTCTGggnytnccncc	(Seq. ID NO. 30)
CAAATTCTTTATACCAAGTCggnggnarncc	(Seq. ID NO. 31)
CCATATATCGCATTTCAGCTgwngwrtccca	(Seq. ID NO. 32)
GGTCGTGGCCAAGgcntggrynga	(Seq. ID NO. 33)

GGCCGGTCCTGggnytsccncc (Seq. ID NO. 34)
TCCTTGTACCAGGTCggnggsarncc (Seq. ID NO. 35)
GCGCATTTCGGCGswnswrtccca (Seq. ID NO. 36).

6. A protein sequence which is required for constructing the activity of a nitrile hydratase and which has less than 100% homology, at the amino acid level, with such known protein sequences, with the nucleic acid sequences encoding it being generated from part sequences which give a positive hybridization signal, under stringent conditions, with the primers exhibiting the nucleic acid sequences of claim 1.

7. A nucleic acid sequence which encodes a protein sequence as claimed in claim 6.

8. An expression system which exhibits one or more nucleic acid sequences as claimed in claim 7.

9. A nitrile hydratase which exhibits protein sequences for α subunits and β subunits as claimed in claim 6.

10. The use of the nucleic acid sequences as claimed in claim 7 for producing improved protein sequences which are required for constructing the activity of a nitrile hydratase.

11. The use of the nitrile hydratases as claimed in claim 9 for preparing organic acid amides and acids.